

Application No.: 10/800,024  
 Filed: March 12, 2004

### AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application:

#### Listing of Claims:

1. (Currently amended) A composition comprising a protein in crystalline form wherein ~~at least a portion of the protein has at least 90% identity with~~ consists of residues 24-292 of SEQ. ID No. 1 ~~SEQ ID NO:1,~~ and wherein the protein crystal has a crystal lattice in a  $P2_1$  space group and unit cell dimensions,  $\pm 5\%$ , of  $a=56.4 \text{ \AA}$ ,  $b=152.5 \text{ \AA}$ ,  $c=73.8 \text{ \AA}$ ,  $\alpha=90.0^\circ$ ,  $\beta=92.2^\circ$ , and  $\gamma=90.0^\circ$ .

2-3. (Cancelled)

4. (Original) A composition according to claim 1 wherein the protein crystal diffracts X-rays for a determination of structure coordinates to a resolution greater than 3.0 Angstroms.

5-8 (Cancelled)

9. (Withdrawn – currently amended) A composition comprising a protein in crystalline form wherein ~~at least a portion of the protein has at least 90% identity with~~ consists of residues 24-258 of SEQ. ID No. 1 ~~SEQ ID NO:1,~~ and wherein the protein crystal has a crystal lattice in a  $P3_121$  space group and unit cell dimensions,  $\pm 5\%$ , of  $a=86.2 \text{ \AA}$ ,  $b=86.2 \text{ \AA}$ ,  $c=146.7 \text{ \AA}$ ,  $\alpha=90.0^\circ$ ,  $\beta=90.0^\circ$ , and  $\gamma=120^\circ$ .

10-11. (Cancelled)

12. (Withdrawn) A composition according to claim 9 wherein the protein crystal diffracts X-rays for a determination of structure coordinates to a resolution greater than 3.0 Angstroms.

13-16. (Cancelled)

17. (Withdrawn – currently amended) A composition comprising a protein in crystalline form wherein ~~at least a portion of the protein has at least 90% identity with~~ consists of residues 24-267 of SEQ. ID No. 1 ~~SEQ ID NO:1,~~ and wherein the protein crystal has a crystal lattice in a  $P4_12_12$  space group and unit cell dimensions,  $\pm 5\%$ , of  $a=114 \text{ \AA}$ ,  $b=114 \text{ \AA}$ ,  $c=157 \text{ \AA}$ ,  $\alpha=90^\circ$ ,  $\beta=90^\circ$ , and  $\gamma=90^\circ$ .

18- 19. (Cancelled)

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20. (Withdrawn) A composition according to claim 17 wherein the protein crystal diffracts X-rays for a determination of structure coordinates to a resolution greater than 3.0 Angstroms.

21-24. (Cancelled)

25. (Currently amended) A method for forming a crystal of a protein comprising:

forming a crystallization volume comprising [::] a precipitant solution and a protein wherein the protein has at least 90% identity with consists of residues 24-292 of SEQ. ID No. 1 SEQ ID NO:1, and wherein the protein crystal has a crystal lattice in a P2<sub>1</sub> space group and unit cell dimensions, +/- 5%, of a=56.4 Å, b=152.5 Å, c=73.8 Å,  $\alpha$ =90.0°,  $\beta$ =92.2°, and  $\gamma$ =90.0°; and

storing the crystallization volume under conditions suitable for crystal formation of the protein.

26-27. (Cancelled)

28. (Original) A method according to claim 25 wherein the protein diffracts X-rays for a determination of structure coordinates to a resolution greater than 3.0 Angstroms.

29-31. (Cancelled)

32. (Original) A method according to claim 25, the method further comprising diffracting the protein crystal to produce a diffraction pattern and solving the structure of the protein from the diffraction pattern.

33. (Withdrawn – currently amended) A method for forming a crystal of a protein comprising:

forming a crystallization volume comprising [::] a precipitant solution and a protein wherein the protein has at least 90% identity with consists of residues 24-258 of SEQ. ID No. 1 SEQ ID NO:1, and wherein the protein crystal has a crystal lattice in a P3<sub>2</sub>1 space group and unit cell dimensions, +/- 5%, of a=86.2 Å, b=86.2 Å, c=146.7 Å,  $\alpha$ =90.0°,  $\beta$ =90.0°, and  $\gamma$ =120°; and

storing the crystallization volume under conditions suitable for crystal formation of the protein.

34- 35. (Cancelled)

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36. (Withdrawn) A method according to claim 33 wherein the protein diffracts X-rays for a determination of structure coordinates to a resolution greater than 3.0 Angstroms.

37- 39. (Cancelled)

40. (Withdrawn) A method according to claim 33, the method further comprising diffracting the protein crystal to produce a diffraction pattern and solving the structure of the protein from the diffraction pattern.

41. (Withdrawn – currently amended) A method for forming a crystal of a protein comprising:  
forming a crystallization volume comprising ~~[[:]~~ a precipitant solution and a protein ~~wherein the protein has at least 90% identity with~~ consists of residues 24-267 of SEQ. ID No. 1 SEQ ID NO:1, and wherein the protein crystal has a crystal lattice in a P4<sub>2</sub>2<sub>1</sub>2 space group and unit cell dimensions,  $\pm 5\%$ , of  $a=114 \text{ \AA}$ ,  $b=114 \text{ \AA}$ ,  $c=157 \text{ \AA}$ ,  $\alpha=90^\circ$ ,  $\beta=90^\circ$ , and  $\gamma=90^\circ$ ; and  
storing the crystallization volume under conditions suitable for crystal formation of the protein.

42- 43. (Cancelled)

44. (Withdrawn) A method according to claim 41 wherein the protein diffracts X-rays for a determination of structure coordinates to a resolution greater than 3.0 Angstroms.

45-47. (Cancelled)

48. (Withdrawn) A method according to claim 41, the method further comprising diffracting the protein crystal to produce a diffraction pattern and solving the structure of the protein from the diffraction pattern.

49. (Currently amended) A ~~composition comprising an isolated~~ protein consisting of residues 24-292 of ~~SEQ. ID No. 1~~ SEQ ID NO:1.

50. (Currently amended) A ~~protein composition~~ according to claim 49 wherein the protein is expressed from a nucleic acid molecule that comprises ~~SEQ. ID No. 2~~ SEQ ID NO:2.

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51. (Withdrawn – currently amended) A ~~composition comprising an isolated~~ protein consisting of residues 24-258 of ~~SEQ-ID No. 4~~ SEQ ID NO:1.

52. (Withdrawn – currently amended) A ~~protein composition~~ according to claim 51 wherein the protein is expressed from a nucleic acid molecule that comprises ~~SEQ-ID No. 3~~ SEQ ID NO:3.

53. (Withdrawn – currently amended) A ~~composition comprising an isolated~~ protein consisting of residues 24-267 of ~~SEQ-ID No. 4~~ SEQ ID NO:1.

54. (Withdrawn – currently amended) A ~~protein composition~~ according to claim 53 wherein the protein is expressed from a nucleic acid molecule that comprises ~~SEQ-ID No. 4~~ SEQ ID NO:4.

55. (Currently amended) A ~~composition comprising an isolated~~ protein consisting of ~~SEQ-ID No. 5~~ SEQ ID NO:5.

56. (Withdrawn) A ~~composition comprising an isolated~~ protein consisting of ~~SEQ-ID No. 6~~ SEQ ID NO:6.

57. (Withdrawn – currently amended) A ~~composition comprising an isolated~~ protein consisting of ~~SEQ-ID No. 7~~ SEQ ID NO:7.

58. (Withdrawn – currently amended) A method of identifying an entity that associates with a protein comprising:

taking structure coordinates from diffraction data obtained from a crystal of a protein that ~~has at least 90% identity with~~ consists of residues 24-292 of ~~SEQ-ID No. 4~~ SEQ ID NO:1, and wherein the protein crystal has a crystal lattice in a P2<sub>1</sub> space group and unit cell dimensions, +/- 5%, of a=56.4 Å, b=152.5 Å, c=73.8 Å,  $\alpha = 90.0^\circ$ ,  $\beta = 92.2^\circ$ , and  $\gamma = 90.0^\circ$ ; and

performing rational drug design using a three dimensional structure that is based on the obtained structure coordinates.

59-60. (Cancelled)

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61. (Withdrawn) A method according to claim 58, the method further comprising selecting one or more entities based on the rational drug design and contacting the selected entities with the protein.

62. (Withdrawn) A method according to claim 58, the method further comprising measuring an activity of the protein when contacted with the one or more entities.

63. (Withdrawn) A method according to claim 58, the method further comprising comparing activity of the protein in the presence of and in the absence of the one or more entities; and selecting entities where activity of the protein changes depending upon whether a particular entity is present.

64. (Withdrawn) A method according to claim 58, the method further comprising contacting cells expressing the protein with the one or more entities and detecting a change in a phenotype of the cells when a particular entity is present.

65. (Withdrawn – currently amended) A method of identifying an entity that associates with a protein comprising:

taking structure coordinates from diffraction data obtained from a crystal of a protein ~~that has at least 90% identity with~~ consists of residues 24-258 of SEQ. ID No. 1 SEQ ID NO:1, and wherein the protein crystal has a crystal lattice in a P3<sub>1</sub>21 space group and unit cell dimensions, +/- 5%, of a=86.2 Å, b=86.2 Å, c=146.7 Å,  $\alpha=90.0^\circ$ ,  $\beta=90.0^\circ$ , and  $\gamma=120^\circ$ ; and

performing rational drug design using a three dimensional structure that is based on the obtained structure coordinates.

66-67. (Withdrawn)

68. (Withdrawn) A method according to claim 65, the method further comprising selecting one or more entities based on the rational drug design and contacting the selected entities with the protein.

69. (Withdrawn) A method according to claim 65, the method further comprising measuring an activity of the protein when contacted with the one or more entities.

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70. (Withdrawn) A method according to claim 65, the method further comprising comparing activity of the protein in the presence of and in the absence of the one or more entities; and selecting entities where activity of the protein changes depending upon whether a particular entity is present.

71. (Withdrawn) A method according to claim 65, the method further comprising contacting cells expressing the protein with the one or more entities and detecting a change in a phenotype of the cells when a particular entity is present.

72. (Withdrawn – currently amended) A method of identifying an entity that associates with a protein comprising:

taking structure coordinates from diffraction data obtained from a crystal of a protein ~~that has at least 90% identity with~~ consists of residues 24-267 of ~~SEQ ID No. 1~~ SEQ ID NO:1, and wherein the protein crystal has a crystal lattice in a  $P4_12_12$  space group and unit cell dimensions,  $\pm 5\%$ , of  $a=114 \text{ \AA}$ ,  $b=114 \text{ \AA}$ ,  $c=157 \text{ \AA}$ ,  $\alpha=90^\circ$ ,  $\beta=90^\circ$ , and  $\gamma=90^\circ$ ; and

performing rational drug design using a three dimensional structure that is based on the obtained structure coordinates.

73-74. (Cancelled)

75. (Withdrawn) A method according to claim 72, the method further comprising selecting one or more entities based on the rational drug design and contacting the selected entities with the protein.

76. (Withdrawn) A method according to claim 72, the method further comprising measuring an activity of the protein when contacted with the one or more entities.

77. (Withdrawn) A method according to claim 72, the method further comprising comparing activity of the protein in the presence of and in the absence of the one or more entities; and selecting entities where activity of the protein changes depending upon whether a particular entity is present.

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78. (Withdrawn) A method according to claim 72, the method further comprising contacting cells expressing the protein with the one or more entities and detecting a change in a phenotype of the cells when a particular entity is present.